

# ENTERED



PCT

## RAW SEQUENCE LISTING

DATE: 03/27/2003

PATENT APPLICATION: US/09/646,569A

TIME: 13:16:44

Input Set : N:\CrF4\03272003\I646569.raw

Output Set: N:\CRF4\03272003\I646569A.raw

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1 <110> APPLICANT: The Trustees of Columbia University in the City of New York
2 <120> TITLE OF INVENTION: Novel Tumor-Associated Marker
3 <130> FILE REFERENCE: 0575/60240-PCT
4 <140> CURRENT APPLICATION NUMBER: US/09/646,569A
5 <141> CURRENT FILING DATE: 2001-09-18
6 <160> NUMBER OF SEQ ID NOS: 28
7 <170> SOFTWARE: PatentIn version 3.1
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19 35 40 45
20 Pro Pro Pro Pro Ala Leu Arg Pro Arg Leu Val Phe His Thr Gln Leu
21 50 55 60
22 Ala His Gly Ser Pro Thr Gly Arg Ile Glu Gly Phe Thr Asn Val Lys
23 65 70 75 80
24 Glu Leu Tyr Gly Lys Ile Ala Glu Ala Phe Arg Leu Pro Thr Ala Glu
25 85 90 95
26 Val Met Phe Cys Thr Leu Asn Thr His Lys Val Asp Met Asp Lys Leu
27 100 105 110
28 Leu Gly Gly Gln Ile Gly Leu Glu Asp Phe Ile Phe Ala His Val Lys
29 115 120 125
30 Gly Gln Arg Lys Glu Val Glu Val Phe Lys Ser Glu Asp Ala Leu Gly
31 130 135 140
32 Leu Thr Ile Thr Asp Asn Gly Ala Gly Tyr Ala Phe Ile Lys Arg Ile
33 145 150 155 160
34 Lys Glu Gly Ser Val Ile Asp His Ile His Leu Ile Ser Val Gly Asp
35 165 170 175
36 Met Ile Glu Ala Ile Asn Gly Gln Ser Leu Leu Gly Cys Arg His Tyr
37 180 185 190
38 Glu Val Ala Arg Leu Leu Lys Glu Leu Pro Arg Gly Arg Thr Phe Thr
39 195 200 205
40 Leu Lys Leu Thr Glu Pro Arg Lys Ala Phe Asp Met Ile Ser Gln Arg
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42 Ser Ala Gly Gly Arg Pro Gly Ser Gly Pro Gln Leu Gly Thr Gly Arg
43 225 230 235 240
44 Gly Thr Leu Arg Leu Arg Ser Arg Gly Pro Ala Thr Val Glu Asp Leu

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49          275          280          285
50    Glu Leu Gly Lys Asp Lys Arg Asn Pro Asp Glu Leu Ala Glu Ala Leu
51          290          295          300
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64    cccctctag  tggaaaatga ggaggctgag ccaggccgtg gagggtctgg cgtggggggag      180
65    ccagggcctt tgggcggagg tgggtcgggg ggcggcgaaa tgggcttgcc cccctcccc      240
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72    atcagcgtgg gcgacatgat cgaggccatt aacgggcaga gcctgctggg ctgccggcac      660
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100	ctgtgaccac cctgtgacc cctgcaggcc acggccaccc agaggccaac tccaatgaga	300
101	agcatccatc ccagcaggac acgcggcctg ctgaacagag cctagacatg gaggagaagg	360
102	actacagtga ggccgatggc ctttcggaga ggaccacgcc cagcaaggcc cagaaatcgc	420
103	cccagaagat tgccaagaaa tacaagagtg ccatctgccg ggtcactctg cttgatgcct	480
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105	gtgaacacct caacctccta gagaaggact acttcggcct gaccttctgt gatgctgaca	600
106	gccagaagaa ctggctggac cctccaagg agatcaagaa gcagatccgg agtagccctt	660
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111	cccgggagct ggaggagagg atcatggagc tgcataagac atatatgggg atgaccccg	960
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116	agagcacaat tggctttaag ctcccaaac accggtcagc caagagactg tggaggtct	1260
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193	ccatgtgaca	tcaggctatc	cccattcccc	ctcttgggcc	tcagtttccc	gacttgcaaa	5880
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212   35          40          45
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214   50          55          60
215   Lys Lys Ala Gln Glu Glu Ala Pro Gln Gln Pro Glu Ala Ala Ala Ala
216   65          70          75          80
217   Val Thr Thr Pro Val Thr Pro Ala Gly His Gly His Pro Glu Ala Asn
218   85          90          95
219   Ser Asn Glu Lys His Pro Ser Gln Asp Thr Arg Pro Ala Glu Gln Ser
220   100         105         110
221   Leu Asp Met Glu Glu Lys Asp Tyr Ser Glu Ala Asp Gly Leu Ser Glu
222   115         120         125
223   Arg Thr Thr Pro Ser Lys Ala Gln Lys Ser Pro Gln Lys Ile Ala Lys
224   130         135         140
225   Lys Tyr Lys Ser Ala Ile Cys Arg Val Thr Leu Leu Asp Ala Ser Glu
226   145         150         155         160
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228   165         170         175
229   Leu Val Cys Glu His Leu Asn Leu Leu Glu Lys Asp Tyr Phe Gly Leu
230   180         185         190
231   Thr Phe Cys Asp Ala Asp Ser Gln Lys Asn Trp Leu Asp Pro Ser Lys
232   195         200         205
233   Glu Ile Lys Lys Gln Ile Arg Ser Ser Pro Trp Asn Phe Ala Phe Thr
234   210         215         220
235   Val Lys Phe Tyr Pro Pro Asp Pro Ala Gln Leu Thr Glu Asp Ile Thr
236   225         230         235         240
237   Arg Tyr Tyr Leu Cys Leu Gln Leu Arg Ala Asp Ile Ile Thr Gly Arg
238   245         250         255
239   Leu Pro Cys Ser Phe Val Thr His Ala Leu Leu Gly Ser Tyr Ala Val
240   260         265         270
241   Gln Ala Glu Leu Gly Asp Tyr Asp Ala Glu Glu His Val Gly Asn Tyr
242   275         280         285
243   Val Ser Glu Leu Arg Phe Ala Pro Asn Gln Thr Arg Glu Leu Glu Glu
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 23,42,48,1105

Seq#:17; N Pos. 23,42

**VERIFICATION SUMMARY**

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L:885 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0

M:341 Repeated in SeqNo=15

L:953 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0